

1990

1	GTGACTCATGCTGTTGAACTTACTGTCAACAGCACTGTAACCTCATGCCTGAGCCAAGC	60
61	TTGTCTAACACGTATATTTTCTCTGTAAAGCACATCACAGCCTTTCTGCACTTAGGAACA	120
121	TTAGACAGCACTTCAGCAGTACACTTGGGGGCCATTTTAAACAATTAAATCACTGATAGG	180
181	CTCCGCTCCGCTCAGGGCGGGCCCCAGACACGGGTTTCCCATGGCAGCACCACGGGCACGCC	240
241	CGGCGCACCTGCTGCCCCGAACCCCTGGCTCCAGGGGGCAATGAGGGGGCAGTGGAAGGG	300
301	GCACTACTCCTCGGGCATTGCCTAGAGAAGCGAGACCGTCCCGCCCTCCCGCTGGCCCTC	360
361	CTTCTCTCCCGCCCGGGGCGCGCAATTCTCCGCCAGAGGGACAGTCGGCCTCATATGT	420
1		M L 2
421	TAAGACCTCTGATCACTAGATCCCCTGCATCTCCACTGAACAACCAAGGCACCCCTACTC	480
3	R P L I T R S P A S P L N N Q G T P T P	22
481	CGGCACAACCTCACAAAATCCAATGCGCATGTCCACACTGATGTGGGCAGCCACATGTACA	540
23	A Q L T K S N <u>A H V H T D V G S H M Y T</u>	42
541	CCAGCAGCCTGGCCACCCTCACCAAATACCCTGTATCCAGAATCAGAAGACTTTGTGATG	600
43	<u>S S L A T L T K Y P V S R I R R L C D G</u>	62
601	GTACAGAGCCCATAGTTTTGGACAGTCTCAAACAGCACTATTTCACTGACAGAGATGGAC	660
63	<u>T E P I V L D S L K Q H Y F T D R D G Q</u>	82
661	AGATGTTTCAATATATCTTGAATTTTCTACGAACATCCAAACTCCTCATTCTTGATGATT	720
83	<u>M F R Y I L N F L R T S K L L I L D D F</u>	102
721	TCAAGGACTACACTTTGTTATATGAAGAGGCAAAATATTTTCAGCTTCAGCCCATGTTGT	780
103	<u>K D Y T L L Y E E A K Y F Q L Q P M L L</u>	122
781	TGGAGATGGAAGATGGAAGCAGGACAGAGAACTGGTCGCTTTTCAAGGCCCTGTGAGT	840
123	<u>E M E R W K Q D R E</u> T G R F S R P C E C	142
841	GCCTTGTTTGTGTGGCCCCAGACCTCAGAGAAAGGATCACGCTAAGTGGTGACAAATCCT	900
143	L V C V A P D L R E R I T L S G D K S L	162
901	TGGTAGAAGAAGTGTTTCCAGAGATCGGCGATGTGATGTGCAACTTTATCAGTGCAGGCT	960
163	V E E V F P E I G D V M C N F I S A G W	182

[illegible]

Figure 2

1 50

K+betaM3 (1) -----
MECHP-2 (1) -----
KCNMB1 (1) -----
CG10465 (1) -----
CG10440 (1) MDRERERDVKALEPRDLSSSTGRIYARSDIKISSSPTVSPTISNSSSPTPT

51 100

K+betaM3 (1) -----MLRRLITRSPASPTNNQ-----GTPTPAQ
MECHP-2 (1) -----MSRRLITRSPASPTNNQ-----GIPTPAQ
KCNMB1 (1) -----
CG10465 (1) -----MSFSMSGD-----HKILL
CG10440 (51) PPASSSVTPGLPGAVAATAAVGGASSAGASSYLHGNHKPITGIPCVA

101 150

K+betaM3 (25) LTKSNAHVHTDVGSHMYTSSLATLTLYPVSRIIRLCDGTEPIVLDSLKQH
MECHP-2 (25) LTKSNAHVHTDVGSHMYTSSLATLTLYPVSRIIRLCDGTEPIVLDSLKQH
KCNMB1 (1) -----LVVKQLVMAQKRCEPTRALCLGVTMVCAVTITYYLLVITVSLPLYQ
CG10465 (14) KCHSSQYLKLNVGGLHYITIGTLTKNNDTMTSAMFSCRMEVLTDS-EGW
CG10440 (101) ASRYTAPVHTDVGGTITYTSSLETLTLYPESKIAKLFNGQTPIVLDSLKQH

151 200

K+betaM3 (75) YFTDRDGMFRMILNFLRTSKLLILDDEFKDYTLLEYEAKYEQLOPMLLEM
MECHP-2 (75) YFIDRDGMFRMILNFLRTSKLLIPDEFKDYTLLEYEAKYEQLOPMLLEM
KCNMB1 (44) KSVWTOESKCHLIETNIRDOELKGGKVPOYPCLVNVSAAGRWAVLYHT
CG10465 (63) ILIDRCCNHFGIILNMLRDGTVPFPEPTNKEIAELLAEAKYCTITELATSC
CG10440 (151) YFIDRDGMFRMILNFMNRNRLLIADDEPDLELLEYEARYEVEPEPMKQIL

201 250

K+betaM3 (125) ERWKQDRETG-----RFSRPCECLVC-----
MECHP-2 (125) ERWKQDRETG-----RFSRPCECLVVR-----
KCNMB1 (94) EDTRDQONQQC-----S-----
CG10465 (113) ERALYAHQEPKPICRIPLITSQ--KEEQLLLSVSLKPAVILVQRQNNKY
CG10440 (201) ESMRKDRVRNGNYLVAPPTPPARHIKTSPTSASPECNYEVVALH-----

251 300

K+betaM3 (146) -----VAPDLRERITLSCDKS-----LVEEVFP
MECHP-2 (147) -----VAPDLGERITLSCDKS-----LVEEVFP
KCNMB1 (105) -----YIPGSVDNYQTARADVKK-----VRAKFQ
CG10465 (161) SYTSTSDNLLKNIELFDKLSLRNERILFIKDVIGPSEICCSWSEYGHGK
CG10440 (246) -----LSPDLGERIMLSARA-----LIDELFP

301 350

K+betaM3 (169) EIGDVMCNFTS-AGWNH-----DSTHIMRFLPSGYCHLNSVQVLERLQQ
MECHP-2 (170) EIGDVMCNFTS-AGWNH-----DSTHIMRFLPSGYCHLNSVQVLERLQQ
KCNMB1 (129) EQQVFYCFSSAP---R-GNE-----TSVLRQRLYGPQALLFSFWPTFLIT
CG10465 (211) KVAELVCTSTIVYATDRKHTKVEFPETARYEETLQVLLYENRNAPDOELMQ
CG10440 (269) EASQATQSSRSQVSWNOG----DWGQITREPLNGYCKLNSVQVLTRELN

351 395

K+betaM3 (212) RGFETVGSRCRGGVGSS-----
MECHP-2 (213) RGFETVGSRCGGVDSSQFSEYVLRRELRRTPRVPSVIRIKQEPD
KCNMB1 (170) GCLLITLMAVKS-----NOYLSITLAAQK
CG10465 (261) ATSSARVGSASGTSINOYTSDEEEERTGLARLRSNKRNNPS-----
CG10440 (314) AGFTIEASVCG-----QGFSEYLLARRVPM-----

Figure 3

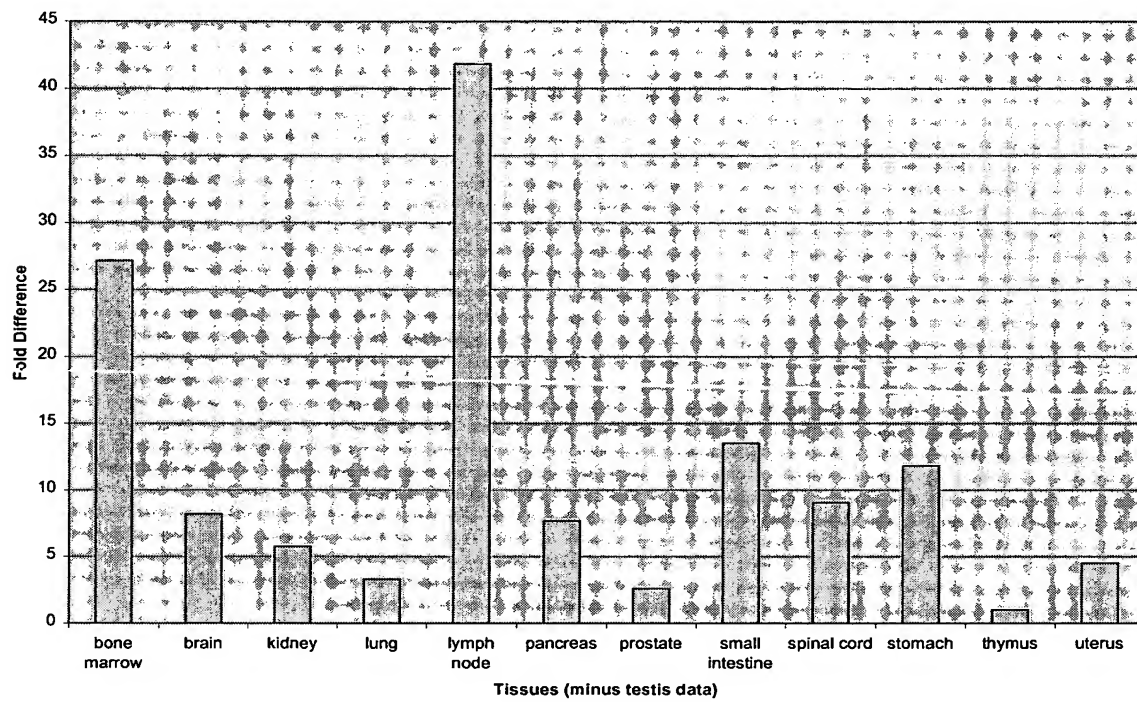


Figure 4.

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
Human membrane channel protein-2	gi Y70452	90.7%	92.5%
Human Maxi-K potassium channel beta subunit	gi 4758625	32.0%	32.0%
Drosophila CG10440 protein	gi 7291303	33.1%	42.6%
Drosophila CG10465 protein	gi 17946205	24.0%	38.8%

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